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; Sequence 3, Application US/08073384C
; Patent No. 5541311
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; APPLICANT: Dahlberg, James E.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.

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; TITLE OF INVENTION: POLYMERASE

; CORRESPONDENCE ADDRESS:

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;      ADDRESSEE:  HAVERSTOCK, MEDLEN & CARROLL
;      STREET:    220 Montgomery Street, Suite 2200
;      CITY:      San Francisco
;      STATE:     California
;      COUNTRY:   United States of America
;      ZIP:       94104
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:     IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:     PatentIn Release #1.0, Version #1.25

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APPLICATION NUMBER: US/08/073,384C

; CLASSIFICATION: 536

APPLICATION NUMBER: US 07/986,330

; ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,837

; TELECOMMUNICATION INFORMATION:

TELEFAX: 415/397-8338

; INFORMATION FOR SEO ID NO:

## ; LENGTH: 2504 base pairs

; TYPE: nucleic acid

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; STRANDEDNESS: double
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;      TOPOLOGY:  linear
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; MOLECULE TYPE: DNA (genomic)

Query Match 1.8%; Score 38.2; DB 1; Length 2504;  
Best Local Similarity 47.7%; Pred. No. 0.54;  
Matches 112; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Yq 722 CAGGACCCCTGCTCATGGGGCTGTTTCCTACTAACCCTAAAGAGAAGACCCAGGAGGAA 781  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1474 CTGGAAAGGGTGCTCCTTGTACGAGCTTAGGCTTCCCCTTGGGGAAGACGCAAAAGACA 1533

Qy 782 CCCCCTGGCCAGAGCAGGGCCCCCTGTGTTGACCGTGGTGTCCAAGTTCAAGGCCTCACTG 841  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1534 GGCAAGCGCTCCACCAGCGCCGCGGTGCTGGAGGCCCTACGGGAGGCCACCCCATCGTG 1593

Qy 842 GAGCAGCTTCTGCAGGTCCCTACACAGCACCACGCCCCACTACATTCGCTGCATCAAGCCC 901  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1594 GAGAAGATCCTCCAGCACCGGGAGCTACCAAGCTCAAGAACACCTACGTGGACCCCCTC 1653

Qy 902 AACAGCCAGGGCCAGGCGCAGACCTTTCTCCAAGAGGAGGTCCTGAGCCAGCTGG 956  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1654 CCAAGCCTCGTCCACCCGAGGACGGGCCGCTCCACACCCGCTTCAACCAGACGG 1708

RESULT 4

US-08-306-691B-46

; Sequence 46, Application US/08306691B

; Patent No. 5734039

; GENERAL INFORMATION:

; APPLICANT: Calabretta, Bruno

; APPLICANT: Skorski, Tomasz

; TITLE OF INVENTION: ANTISENSE

; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.

; STREET: Two Penn Center, Suite 1800

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/306,691B

; FILING DATE: September 15, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 8321-8

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383

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; TELEX: No. 5734039e

; INFORMATION FOR SEQ ID NO: 46:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2638 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-306-691B-46

Alignment Scores:

Pred. No.:	0.0454	Length:	2638
Score:	124.00	Matches:	141
Percent Similarity:	32.45%	Conservative:	55
Best Local Similarity:	23.34%	Mismatches:	227
Query Match:	3.81%	Indels:	181
DB:	1	Gaps:	27

US-09-830-914C-1 (1-612) x US-08-306-691B-46 (1-2638)

Qy 87 HisTyrLeuArgAlaGlnGlnGluGluTyrAlaValGluGlyLeuGluTrpSerPheIle 106

|||:::||||| ||| ||| ::| ::|

Db 559 CATCATCTGCGAGGCCACACAAGGTGCTGGGCAACCGCTGGGCCGAGATCGCCAAGATGTT 618  
 Qy 107 AsnTyrGlnAspAsnGlnProCys-----LeuAspLeuIleGluGlySerProIle 123  
 :::||| ||| ||| |||:::|  
 Db 619 GCCAGGGAGGACAGACAATGCTGTGAAGAATCACTGGAAGCTCTACCATCAAAGGAAGGT 678  
 Qy 124 SerIleCysSerLeuIleAsnGluGluCysArgLeuAsnArgProSer----- 139  
 |||::: ||||| |||||  
 Db 679 GGACACAGGAGGCTTCTTGAGCGAGTCCAAAGACTGCAAGCCCCAGTGTACTTGCTGCT 738  
 Qy 140 SerAlaArgGlnLeuGlnThrArgIleGluThrAlaLeuAlaGlySerProCysLeuGly 159  
 ||||| ||| ||| |||  
 Db 739 GGAGCTCGAGGACAAGGACGGCCTCCAGAGTGCCCGAGCCACGGAAGGCCAGGGAAGTCT 798  
 Qy 160 HisAsnLysLeuSerArgGluProSerPheIleValValHisTyrAlaGlyProValArg 179  
 :::::|::: |||||::: ||| ||| :::  
 Db 799 TCTGACCAACTGGCCCTCCGTCCTCCTAC-----CATAAAGGAGGAGGAAAACAG 849  
 Qy 180 -TyrHis-----ThrAlaGlyLeuValGluLysAsnLysAspProIleProProGluLe 197  
 ||| ||| :::::||||| :::|  
 Db 850 TGAGGAGGAAGTTGCAGCAGCCACCACATCGAAGGAACAGGAGCCCATCGGTACAGATCT 909  
 Qy 197 uThrArgLeuLeuGlnGlnSerGlnAspProLeuLeuMetGlyLeuPheProThrAsnPr 217  
 | ::: :::: :::| ||||| ||  
 Db 910 GGACGCAGTG-----CGAACACCAGAGCCCTTG-----GAGGAATTCCC 948  
 Qy 217 oLysGluLysThrGlnGluGluProProGlyGlnSerArgAlaProValLeuThrValVa 237  
 |||| ::: ||||| ||| :::: ||| |||||  
 Db 949 GAAGCGTGAGGACCAGGAAGGCTCCCCACCAGAAACGAGCCTGCCTTACAAGTGGGTGGT 1008  
 Qy 237 lSerLysPheLys-----AlaSerLeuGluGlnLeuLeuGlnVa 250  
 | :::| ||||| ::: ||| ::  
 Db 1009 GGAGGCAGCTAACCTCCTCATCCCCGCTGTGGGTCTAGCCTCTCTGAAGCCCTGGACTT 1068  
 Qy 250 lLeuHisSerThrThrProHisTyrIleArgCysIleLys----- 263  
 ::: ||| ::: |||  
 Db 1069 GATCGAGTCGGACCCTGATGCTTGGTGTGACCTGAGTAAATTTGACCTCCCTGAGGAACC 1128  
 Qy 264 -----ProAsnSerGlnGlyGlnAlaGlnThrPheLeuGlnGluGl 277  
 ||||| ||| ||| |||:::|  
 Db 1129 ATCTGCAGAGGACAGTATCAACAACAGCCTAGTGAGCTGCAAGCGTCACATCAGCAGCA 1188  
 Qy 277 uValLeuSerGlnLeuGluAlaCysGlyLeuVal----- 288  
 :|| |||| ::: |||||  
 Db 1189 AGTCCTGCCACCCCGCCAGCCTTCCGCCCTGGTGCCAGTGTGACCGAGTACCGCCTGGA 1248  
 Qy 289 -----GluThrIleHisIleSerAl 295  
 ||| ||| |||||  
 Db 1249 TGGCCACACCATCTCAGACCTGAGCCGGAGCAGCCGGGGCGAGCTGATCCCCATCTCCCC 1308  
 Qy 295 aAla-----GlyPheProIleArgValSerHisArgAsnPh 307  
 ::: ||| ||| ||| |||  
 Db 1309 CAGCACTGAAGTCGGGGGCTCTGGCATTTGGCACACCGCCCTCTGTGCTCAAGCGGCAGAG 1368  
 Qy 307 eValGluArgTyrLysLeu-----LeuArgArgLeuHi 318  
 ||| ||| ||| |||  
 Db 1369 GAAGAGGCGTGTGGCTCTGTCCCTGTCACTGAGAATAGCACCAGTCTGTCTTCTTCTGGA 1428

Qy 318 sProCysThrSerSerGlyProAspSerProTyrProAlaLysGlyLeuPro----- 335  
 ||| ||| ||| ||| ||| ||| ||| |||  
 Db 1429 TTCCTGTAACAGCCTCACGCCCAAGAGCACA---CCTGTTAAGACCCTGCCCTTCTCGCC 1485  
 Qy 336 -----GluTrpCysProHisSerGluGluAlaThrLeuGluProLeuIl 350  
 ||| ::::: ||||| |||  
 Db 1486 CTCCCAGTTTCTGAACTTCTGG-----AACAAACAGGACACATTGGAG---CTGGA 1533  
 Qy 350 eGlnAspIleLeuHisThrLeuProValLeuThrGlnAlaAlaAlaIleThrGlyAspSe 370  
 ||| :: ||||| ::||| ::|||  
 Db 1534 GAGCCCCTCGCTGACATCCACCCAGTGTGCAGCCAGAAGGTGGTGGTCACC----- 1585  
 Qy 370 rAlaGluAlaMetProAlaProMetHisCysGlyArgThrLysValPheMet-ThrAspS 390  
 |||::||| ||| ||| ::||| :  
 Db 1586 -----ACACCACTGCAC-----CGGGACAAGACACCCCTGCACCAGAA 1623  
 Qy 390 erMetLeuGluLeu----- 394  
 ::||| |||  
 Db 1624 ACATGCTGCGTTTGTAAACCCAGATCAGAAGTACTCCATGGACAACACTCCCCACACGCC 1683  
 Qy 395 -----LeuGluCysGlyArgAlaA 401  
 ||| ||| |  
 Db 1684 AACCCCGTTCAAGAACGCCCTGGAGAAGTACGGACCCCTGAAGCCCCTGCCACAGACCCC 1743  
 Qy 401 rgValLeuGluGlnCys---AlaArgCysIleGln-GlyGlyTrpArgArg-----His 417  
 || :: ||||| ||||| ||| |||  
 Db 1744 GCACCTGGAGGAGGACTTGAAGGAGGTGCTGCGTTCTGAGGCTGGCATCGAACTCATCAT 1803  
 Qy 418 ArgHisArgGluGlnGluArgGlnTrpArgAlaValMetLeuIleGlnAlaAlaIleArg 437  
 ||| ||| ||| ||| ::|||  
 Db 1804 CGAGGACGACATCAGGCCCGA-----GAAGCAGAAGAGGAA 1839  
 Qy 438 SerTrp-LeuThrArgLysHisIleGlnArgLeuHisAlaAlaAlaThrValIleLysAr 457  
 ::||| ||| ||| |||::: ::  
 Db 1840 GCCTGGGCTGCGGCGAGCCCCATCAAGAAAGTCCGGAAGTCT----- 1882  
 Qy 457 gAlaTrpGlnLysTrpArgIleArgMetAlaCysLeuAlaAlaLysGluLeuAspGlyVa 477  
 ||||| ::|||  
 Db 1883 -----CTGGCTCTTGACATTGTGGATGAGGA 1908  
 Qy 477 lGluGluLysHisPheSerGlnAlaProCysSerLeuSer-----ThrSerProLe 494  
 :: ||| ||| ||||| |||::: |||  
 Db 1909 TGTGAAGCTGATGATGTCCACACTGCCCAAGTCTCTATCCTTGCCGACAACAGCCCTTC 1968  
 Qy 494 uGlnThrArgLeuLeuGluAlaIleIleArgLeuTrpProLeuGlyLeuValLeuAlaAs 514  
 :: ||| |||:: |||  
 Db 1969 AAACCTCTCCAGCCTCACCTG-----TCAGGTATCAAAGAAGACAA 2010  
 Qy 514 nThrAlaMetGlyValGlySerPheGlnArgLysLeuValValTrpAlaCysLeuGlnLe 534  
 |::: :: ||| ||| ||| ||| |||  
 Db 2011 CAGCTTGCTCAACCAGGGCTTCTTGCAGGCCAAGCCCGAGAAGGCAGCAGTGGCCAGAA 2070  
 Qy 534 uProArgGlySerProSerSerTyrThrValGlnThrAlaGlnAspGlnAla-GlyValT 554  
 ||||| ||| ::||| ||| |||  
 Db 2071 GCCCCGA-----AGCCACTTCACGACACCTGCCCTATGTCCAGTGCCTGGA---- 2117

Qy 554 hrSerIleArgAlaLeuProGlnGly-----SerIleLysPheHisCysArgLysSerP 572  
||| ||| ||| ||| |||::: |  
Db 2118 -----AGACGGTGGCCTGCGGGGGGACCAGGGACCAGCTTTTCATGCAGGAGAAAGC 2169

Qy 572 ro 572  
||  
Db 2170 CC 2171